

1646



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OCT 22 2002

1600

RAW SEQUENCE LISTING

DATE: 10/10/2002

PATENT APPLICATION: US/09/352,570A

TIME: 10:08:11

Input Set : A:\00398.506001.SEQLIST.TXT

Output Set: N:\CRF4\10102002\I352570A.raw

ENTERED

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4 <110> APPLICANT: Michael E. Mendelsohn
7 <120> TITLE OF INVENTION: METHOD FOR ASSAYING COMPOUNDS AFFECTING
8   CELL DIVISION
10 <130> FILE REFERENCE: 00398/506001
12 <140> CURRENT APPLICATION NUMBER: 09/352,570A
13 <141> CURRENT FILING DATE: 1999-07-13
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 618
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)...(618)
28 <400> SEQUENCE: 1
29 atg gcg ctg cag ctc tcc cgg gag cag gga atc acc ctg cgc ggg agc   48
30 Met Ala Leu Gln Leu Ser Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser
31 1 5 10 15
33 gcc gaa atc gtg gcc gag ttc ttc tca ttc ggc atc aac agc att tta   96
34 Ala Glu Ile Val Ala Glu Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu
35 20 25 30
37 tat cag cgt ggc ata tat cca tct gaa acc ttt act cga gtg cag aaa   144
38 Tyr Gln Arg Gly Ile Tyr Pro Ser Glu Thr Phe Thr Arg Val Gln Lys
39 35 40 45
41 tac gga ctc acc ttg ctt gta act act gat ctt gag ctc ata aaa tac   192
42 Tyr Gly Leu Thr Leu Leu Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr
43 50 55 60
45 cta aat aat gtg gtg gaa caa ctg aaa gat tgg tta tac aag tgt tca   240
46 Leu Asn Asn Val Val Glu Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser
47 65 70 75 80
49 gtt cag aaa ctg gtt gta gtt atc tca aat att gaa agt ggt gag gtc   288
50 Val Gln Lys Leu Val Val Val Ile Ser Asn Ile Glu Ser Gly Glu Val
51 85 90 95
53 ctg gaa aga tgg cag ttt gat att gag tgt gac aag act gca aaa gat   336
54 Leu Glu Arg Trp Gln Phe Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp
55 100 105 110
57 gac agt gca ccc aga gaa aag tct cag aaa gct atc cag gat gaa atc   384
58 Asp Ser Ala Pro Arg Glu Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile
59 115 120 125
61 cgt tca gtg atc aga cag atc aca gct acg gtg aca ttt ctg cca ctg   432
62 Arg Ser Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu
63 130 135 140

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RAW SEQUENCE LISTING

DATE: 10/10/2002

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Input Set : A:\00398.506001.SEQLIST.TXT

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65 ttg gaa gtt tct tgt tca ttt gat ctg ctg att tat aca gac aaa gat 480
66 Leu Glu Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp
67 145 150 155 160
69 ttg gtt gta cct gaa aaa tgg gaa gag tcg gga cca cag ttt att acc 528
70 Leu Val Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr
71 165 170 175
73 aat tct gag gaa gtg cgc ctt cgt tca ttt act act aca atc cac aaa 576
74 Asn Ser Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Thr Ile His Lys
75 180 185 190
77 gta aat agc atg gtg gcc tac aaa att cct gtc aat gac tga 618
78 Val Asn Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp *
79 195 200 205
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 199
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 2
89 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
90 1 5 10 15
91 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
92 20 25 30
93 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
94 35 40 45
95 Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Glu
96 50 55 60
97 Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
98 65 70 75 80
99 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
100 85 90 95
101 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
102 100 105 110
103 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
104 115 120 125
105 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
106 130 135 140
107 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
108 145 150 155 160
109 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
110 165 170 175
111 Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala
112 180 185 190
113 Tyr Lys Ile Pro Val Asn Asp
114 195
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 600
119 <212> TYPE: DNA
120 <213> ORGANISM: Ovis aries
122 <220> FEATURE:
123 <221> NAME/KEY: CDS

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124 <222> LOCATION: (1)...(600)

126 <400> SEQUENCE: 3

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127 cgg gag caa ggc atc acc ttg cgc ggg agc gcc gag atc gtg gcc gag 48
128 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
129 1 5 10 15
131 ttc ttc tca ttt ggt atc aac agt att tta tat cag cgt ggc ata tat 96
132 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
133 20 25 30
135 cca tcg gaa acc ttt act cga gtg cag aaa tat gga ctc acc ttg ctt 144
136 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
137 35 40 45
139 gta act act gat cct gag ctc ata aaa tac cta aat aat gtg gtg gat 192
140 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
141 50 55 60
143 caa cta aaa gaa tgg tta tac aag tgt tca gtt cag aaa ctg gtg gta 240
144 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
145 65 70 75 80
147 gtc atc tca aat att gaa agt gga gag gtc ctt gaa aga tgg cag ttt 288
148 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
149 85 90 95
151 gat att gag tgt gac aag act gca aaa gat gac agt gca ccc aga gaa 336
152 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
153 100 105 110
155 aag tct cag aaa gct atc caa gat gaa atc cgt tca gtg atc aga cag 384
156 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
157 115 120 125
159 atc aca gct aca gta aca ttt ctg cca ctg ttg gaa gtt tct tgt tca 432
160 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
161 130 135 140
163 ttt gat ctc ctc att tat aca gac aaa gat ctg gtt gta cct gag aaa 480
164 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
165 145 150 155 160
167 tgg gaa gag tcc gga cca cag ttc att acc aat tct gaa gaa gtt cgt 528
168 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
169 165 170 175
171 ctt cgt tca ttc act act aca att cac aaa gta aat agc atg gta gcc 576
172 Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala
173 180 185 190
175 tac aaa att cct gtc cat gac tga 600
176 Tyr Lys Ile Pro Val His Asp *
177 195

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180 <210> SEQ ID NO: 4

181 <211> LENGTH: 199

182 <212> TYPE: PRT

183 <213> ORGANISM: Ovis aries

185 <400> SEQUENCE: 4

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186 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
187 1 5 10 15
188 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr

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189          20          25          30
190 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
191          35          40          45
192 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
193          50          55          60
194 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
195 65          70          75          80
196 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
197          85          90          95
198 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
199          100         105         110
200 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
201          115         120         125
202 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
203          130         135         140
204 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
205 145         150         155         160
206 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
207          165         170         175
208 Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala
209          180         185         190
210 Tyr Lys Ile Pro Val His Asp
211          195

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214 <210> SEQ ID NO: 5

215 <211> LENGTH: 1458

216 <212> TYPE: DNA

217 <213> ORGANISM: Mus musculus

219 <400> SEQUENCE: 5

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220 atggcattct acagtcctgc tgtgatgaac tacagtgttc ccagcagcac cggtaacctg 60
221 gaaggtgggc ctgttcgcca gactgcaagc ccaaattgtc tatggccaac ttctggacac 120
222 ctctctcctt tagccaccca ctgccaatca tcgttctct atgcagaacc tcaaaagagt 180
223 ccttggtgtg aagcaagatc actagaacac accttgctg taaacagaga gacctgaag 240
224 aggaagcttg gcgggagcgg ttgtgccagc cctgttacta gtccaagcac caagagggat 300
225 gctcacttct gtgccgtctg cagtgtattat gcatctgggt atcattacgg tgtctgggcc 360
226 tgtgaaggat gtaaggcctt ttttaaaaga agcattcaag gacataatga ctatatctgt 420
227 ccagccacga atcagtgtac gatagacaag aaccggcgta aaaactgcca ggcctgccga 480
228 cttcgcaagt gttacgaagt aggaatggtc aagtgtggat ccaggagaga aagggtgtgg 540
229 taccgaatag tacgaagaca gagaagtgcc agcgagcagg tgcatcgctt gaacaaagcc 600
230 aagagaacca gtgggcacac accccgggtg aaggagctac tgctgaactc tctgagtccc 660
231 gagcagctgg tgctcaccct gctggaagct gagccaccca atgtgctagt gagtcgtccc 720
232 agcatgccct tcaccgaggc ctccatgatg atgtccctta cgaagctggc tgacaaggaa 780
233 ctggtgcaca tgattggctg ggccaagaaa atccctggct ttgtggagct cagcctgttg 840
234 gaccaagtcc gcctcttgga aagctgctgg atggagggtg tgatggtggg gctgatgtgg 900
235 cgctccatcg accaccccg caagctcatc tttgtccag acctcgctt ggacagggat 960
236 gaggggaagt gcgtggaagg gattctggaa atctttgaca tgctcctggc gacgacggca 1020
237 cggttcctgt agttaaaact gcagcacaaa gaatatctgt gtgtgaaggc catgattctc 1080
238 ctcaactcca gtatgtacca cttggctacc gcaagccagg aagcagagag tagccggaag 1140
239 ctgacacacc tattgaacgc agtgacagat gccctggctt ggggtgattt gaagagtaga 1200
240 atctcttccc agcagcagtc agtccgtctg gccaaacctc tgatgcttct ttctcatgtc 1260

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Output Set: N:\CRF4\10102002\I352570A.raw

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241 aggcacatca gtaacaaggg catggaacat ctgctcagca tgaagtgcaa aaatgtgggtc 1320
242 ccggtgtacg acctgctgct ggagatgctg aatgctcaca cgcttcgagg gtacaagtcc 1380
243 tcaatctcgg ggtctgggtg ctgctcgaca gaggacagta agagcaaaga gggctcccag 1440
244 aacctccagt ctcaagtga 1458
246 <210> SEQ ID NO: 6
247 <211> LENGTH: 485
248 <212> TYPE: PRT
249 <213> ORGANISM: Mus musculus
251 <400> SEQUENCE: 6
252 Met Ala Phe Tyr Ser Pro Ala Val Met Asn Tyr Ser Val Pro Ser Ser
253 1 5 10 15
254 Thr Gly Asn Leu Glu Gly Gly Pro Val Arg Gln Thr Ala Ser Pro Asn
255 20 25 30
256 Val Leu Trp Pro Thr Ser Gly His Leu Ser Pro Leu Ala Thr His Cys
257 35 40 45
258 Gln Ser Ser Leu Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu
259 50 55 60
260 Ala Arg Ser Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys
261 65 70 75 80
262 Arg Lys Leu Gly Gly Ser Gly Cys Ala Ser Pro Val Thr Ser Pro Ser
263 85 90 95
264 Thr Lys Arg Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser
265 100 105 110
266 Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe
267 115 120 125
268 Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn
269 130 135 140
270 Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Asn Cys Gln Ala Cys Arg
271 145 150 155 160
272 Leu Arg Lys Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg
273 165 170 175
274 Glu Arg Cys Gly Tyr Arg Ile Val Arg Arg Gln Arg Ser Ala Ser Glu
275 180 185 190
276 Gln Val His Cys Leu Asn Lys Ala Lys Arg Thr Ser Gly His Thr Pro
277 195 200 205
278 Arg Val Lys Glu Leu Leu Leu Asn Ser Leu Ser Pro Glu Gln Leu Val
279 210 215 220
280 Leu Thr Leu Leu Glu Ala Glu Pro Pro Asn Val Leu Val Ser Arg Pro
281 225 230 235 240
282 Ser Met Pro Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu
283 245 250 255
284 Ala Asp Lys Glu Leu Val His Met Ile Gly Trp Ala Lys Lys Ile Pro
285 260 265 270
286 Gly Phe Val Glu Leu Ser Leu Leu Asp Gln Val Arg Leu Leu Glu Ser
287 275 280 285
288 Cys Trp Met Glu Val Leu Met Val Gly Leu Met Trp Arg Ser Ile Asp
289 290 295 300
290 His Pro Gly Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp
291 305 310 315 320

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VERIFICATION SUMMARY

DATE: 10/10/2002

PATENT APPLICATION: US/09/352,570A

TIME: 10:08:15

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